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RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/756,247   DATE: 01/25/2001
                                         TIME: 10:36:26

Input Set : A:\es.txt
Output Set: N:\CRF3\01252001\I756247.raw

p.5

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 3 <110> APPLICANT: Godbole, Shubhada D
 4         Boyle, Bryan J
 5         Mize, Nancy K
 6         Deng, Cenhua
 7         Goodrich, Ryle
 8         Arterburn, Matthew C
 9         Zhou, Ping
10         Tang, Y. Tom
11         Liu, Chenghua
12         Yeung, George
13         Drmanac, Radoje T
15 <120> TITLE OF INVENTION: METHODS AND MATERIALS RELATING TO ALPHA-2-MACROGLOBULIN-LIKE POLYPEPTIDES
16         AND POLYNUCLEOTIDES
18 <130> FILE REFERENCE: HYS-31CIP
20 <140> CURRENT APPLICATION NUMBER: US/09/756,247
21 <141> CURRENT FILING DATE: 2001-01-08
23 <150> PRIOR APPLICATION NUMBER: 09/649,167
24 <151> PRIOR FILING DATE: 2000-08-23
26 <150> PRIOR APPLICATION NUMBER: 09/540,217
27 <151> PRIOR FILING DATE: 2000-03-31
29 <150> PRIOR APPLICATION NUMBER: 09/684,711
30 <151> PRIOR FILING DATE: 2000-10-06
32 <150> PRIOR APPLICATION NUMBER: 09/560,875
33 <151> PRIOR FILING DATE: 2000-04-27
35 <150> PRIOR APPLICATION NUMBER: 09/496,914
36 <151> PRIOR FILING DATE: 2000-02-03
38 <160> NUMBER OF SEQ ID NOS: 41
40 <170> SOFTWARE: PatentIn version 3.0
42 <210> SEQ ID NO: 1
43 <211> LENGTH: 386
44 <212> TYPE: DNA
45 <213> ORGANISM: Homo sapiens
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50 atagcaacag gattgcacag ggctggaagt ggtacctgag caaggcattg tatacctgtc     120
52 cttccaactg gcaccagagg caatgctgga cacctacatg tggcagtggc tgagggcaag     180
54 acctttggta cttttcagtgt ggaggaatat gtgctgccga agtttaagga ggatttcgtc    240
56 cacaatccgg gggtcgggag taggaattat tttttgcttt gaggagaaca aaaaggttct     300
58 aattcagagg gggaacggca cctttgtaca gactgacaaa cctctctaca ccccagggca     360
60 gcaagtgtat ttccgcattg tcacca                                          386
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69 tggacaattc ggcacgaget agcaacttct ggactgaaga agaggcactt acattggatc      60
71 tcctttcttg taccacctcc tgctggtggc acagaagaag tggccacaat ccgggtgtcg     120
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 73 ggagttgtga aataacatca gctttgagga gaagaaaaag gttctaattc agaggcaggg   180
 75 gaacggcacc tttgtacaga ctgacaaacc tctctacacc ccagggcagc aagtgtattt   240
 77 ccgcattgtc accatggata gcaacttcgt tccagtgaat gacaagtact ccatggtgga   300
 79 actacaggat ccaaatagca acaggattgc acagtggctg gaagtggtac ctgagcaagg   360
 81 cattgtagac ctgtccttcc aactggcacc agaggcaatg ctgggcacct acactgtggc   420
 83 agtggctgag ggcaagacct ttggtacttt cagtgtggag gaatatgtgc tgccgaagtt   480
 85 taaggtggaa gtggtggaac ccaaggagtt atcaacggtg caggaatctt tcttagtaaa   540
 87 aatttgttgt aggtacacct atggaaagc catgctaggg gcagtgcagg tatctgtgtg   600
 89 tcagaagggc aaatacttac tggtatcgag aggtgggaac gggaaccagc ttcctggacc   660
 91 aatgcaggaa cctctctgga cagactgaca aaacaggatg tttctcagca cctgtggaca   720
 93 tggccacctt tgacctcatt ggatatgcgt acagccatca aatcaatatt gtggctactg   780
 95 ttgtggagga aggqacaggt gtggaggcca atgccactca gaatatctac atttctccac   840
 97 aaatgggatt aaatgacctt tggaagacac cagcaatttt taccatccaa attttcccct   900
 99 tcagtgggga agataaggaa ttaggggcca atgatgacct cttcctcaag aaccatctag   960
101 tgtttctggt gatttatggc acaaatggaa ccttcaacca gaccctggtt actgataaca  1020
103 atggcctagc tccctttacc tttggagaaa tccccggtgg aaagggacag aacgttctct  1080
105 ggaggqaaag ttttcaatag gaaaacttat tatataatcc ggaacaaagg gccaccgtta  1140
107 ctaccaaaaa ggcctaacct gggcctgcga acccttttac aagaacaaac ccggaacttt  1200
109 cctttggcat tccccccggct taaacggccc cttgaaatgt ggccagcccc aggaagtgct  1260
111 ggtggaatta ttacattcga cccgggccat gcaagcccct gacccaagag atcaaccttc  1320
113 ttctactatt ttaaataggg aaaggaagtt tggtgaatg                          1359
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117 <211> LENGTH: 4527
118 <212> TYPE: DNA
119 <213> ORGANISM: Homo sapiens
121 <220> FEATURE:
122 <221> NAME/KEY: CDS
123 <222> LOCATION: (1)..(4527)
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126 atg tgg gct cag ctc ctt cta gga atg ttg gcc cta tca cca gcc att    48
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128 1               5                   10                  15
130 gca gaa gaa ctt cca aac tac ctg gtg aca tta cca gcc cgg cta aat    96
131 Ala Glu Glu Leu Pro Asn Tyr Leu Val Thr Leu Pro Ala Arg Leu Asn
132             20                  25                  30
134 ttc ccc tcc gtt cag aag gtt tgt ttg gac ctg agc cct ggg tac agt   144
135 Phe Pro Ser Val Gln Lys Val Cys Leu Asp Leu Ser Pro Gly Tyr Ser
136         35                  40                  45
138 gat gtt aaa ttc acg gtt act ctg gag acc aag gac aag acc cag aag   192
139 Asp Val Lys Phe Thr Val Thr Leu Glu Thr Lys Asp Lys Thr Gln Lys
140     50                  55                  60
142 ttg cta gaa tac tct gga ctg aag aag agg cac tta cat tgt atc tcc   240
143 Leu Leu Glu Tyr Ser Gly Leu Lys Lys Arg His Leu His Cys Ile Ser
144 65                  70                  75                  80
146 ttt ctt gta cca cct cct gct ggt ggc aca gaa gaa gtg gcc aca atc   288
147 Phe Leu Val Pro Pro Pro Ala Gly Gly Thr Glu Glu Val Ala Thr Ile
148             85                  90                  95
150 cgg gtg tcg gga gtt gga aat aac atc agc ttt gag gag aag aaa aag   336
151 Arg Val Ser Gly Val Gly Asn Asn Ile Ser Phe Glu Glu Lys Lys Lys
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152               100              105              110
154 gtt cta att cag agg cag ggg aac ggc acc ttt gta cag act gac aaa     384
155 Val Leu Ile Gln Arg Gln Gly Asn Gly Thr Phe Val Gln Thr Asp Lys
156           115              120              125
158 cct ctc tac acc cca ggg cag caa gtg tat ttc cgc att gtc acc atg     432
159 Pro Leu Tyr Thr Pro Gly Gln Gln Val Tyr Phe Arg Ile Val Thr Met
160      130              135              140
162 gat agc aac ttc gtt cca gtg aat gac aag tac tcc atg gtg gaa cta     480
163 Asp Ser Asn Phe Val Pro Val Asn Asp Lys Tyr Ser Met Val Glu Leu
164 145              150              155              160
166 cag gat cca aat agc aac agg att gca cag tgg ctg gaa gtg gta cct     528
167 Gln Asp Pro Asn Ser Asn Arg Ile Ala Gln Trp Leu Glu Val Val Pro
168              165              170              175
170 gag caa ggc att gta gac ctg tcc ttc caa ctg gca cca gag gca atg     576
171 Glu Gln Gly Ile Val Asp Leu Ser Phe Gln Leu Ala Pro Glu Ala Met
172           180              185              190
174 ctg ggc acc tac act gtg gca gtg gct gag ggc aag acc ttt ggt act     624
175 Leu Gly Thr Tyr Thr Val Ala Val Ala Glu Gly Lys Thr Phe Gly Thr
176           195              200              205
178 ttc agt gtg gag gaa tat gtg ctg ccg aag ttt aag gtg gaa gtg gtg     672
179 Phe Ser Val Glu Glu Tyr Val Leu Pro Lys Phe Lys Val Glu Val Val
180      210              215              220
182 gaa ccc aag gag tta tca acg gtg cag gaa tct ttc tta gta aaa att     720
183 Glu Pro Lys Glu Leu Ser Thr Val Gln Glu Ser Phe Leu Val Lys Ile
184 225              230              235              240
186 tgt tgt agg tac acc tat gga aag ccc atg cta ggg gca gtg cag gta     768
187 Cys Cys Arg Tyr Thr Tyr Gly Lys Pro Met Leu Gly Ala Val Gln Val
188              245              250              255
190 tct gtg tgt cag aag gca aat act tac tgg tat cga gag gtg gaa cgg     816
191 Ser Val Cys Gln Lys Ala Asn Thr Tyr Trp Tyr Arg Glu Val Glu Arg
192           260              265              270
194 gaa cag ctt cct gac aaa tgc agg aac ctc tct gga cag act gac aaa     864
195 Glu Gln Leu Pro Asp Lys Cys Arg Asn Leu Ser Gly Gln Thr Asp Lys
196           275              280              285
198 aca gga tgt ttc tca gca cct gtg gac atg gcc acc ttt gac ctc att     912
199 Thr Gly Cys Phe Ser Ala Pro Val Asp Met Ala Thr Phe Asp Leu Ile
200      290              295              300
202 gga tat gcg tac agc cat caa atc aat att gtg gct act gtt gtg gag     960
203 Gly Tyr Ala Tyr Ser His Gln Ile Asn Ile Val Ala Thr Val Val Glu
204 305              310              315              320
206 gaa ggg aca ggt gtg gag gcc aat gcc act cag aat atc tac att tct     1008
207 Glu Gly Thr Gly Val Glu Ala Asn Ala Thr Gln Asn Ile Tyr Ile Ser
208           325              330              335
210 cca caa atg gga tca atg acc ttt gaa gac acc agc aat ttt tac cat     1056
211 Pro Gln Met Gly Ser Met Thr Phe Glu Asp Thr Ser Asn Phe Tyr His
212      340              345              350
214 cca aat ttc ccc ttc agt ggg aag ata aga gtt agg ggc cat gat gac     1104
215 Pro Asn Phe Pro Phe Ser Gly Lys Ile Arg Val Arg Gly His Asp Asp
216           355              360              365
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219 Ser Phe Leu Lys Asn His Leu Val Phe Leu Val Ile Tyr Gly Thr Asn
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222 gga acc ttc aac cag acc ctg gtt act gat aac aat ggc cta gct ccc      1200
223 Gly Thr Phe Asn Gln Thr Leu Val Thr Asp Asn Asn Gly Leu Ala Pro
224 385             390             395             400
226 ttt acc ttg gag aca tcc ggt tgg aat ggg aca gac gtt tct ctg gag      1248
227 Phe Thr Leu Glu Thr Ser Gly Trp Asn Gly Thr Asp Val Ser Leu Glu
228             405             410             415
230 gga aag ttt caa atg gaa gac tta gta tat aat ccg gaa caa gtg cca      1296
231 Gly Lys Phe Gln Met Glu Asp Leu Val Tyr Asn Pro Glu Gln Val Pro
232         420             425             430
234 cgt tac tac caa aat gcc tac ctg cac ctg cga ccc ttc tac agc aca      1344
235 Arg Tyr Tyr Gln Asn Ala Tyr Leu His Leu Arg Pro Phe Tyr Ser Thr
236         435             440             445
238 acc cgc agc ttc ctt ggc atc cac cgg cta aac ggc ccc ttg aaa tgt      1392
239 Thr Arg Ser Phe Leu Gly Ile His Arg Leu Asn Gly Pro Leu Lys Cys
240     450             455             460
242 ggc cag ccc cag gaa gtg ctg gtg gat tat tac atc gac ccg gcc gat      1440
243 Gly Gln Pro Gln Glu Val Leu Val Asp Tyr Tyr Ile Asp Pro Ala Asp
244 465             470             475             480
246 gca agc cct gac caa gag atc agc ttc tcc tac tat tta ata ggg aaa      1488
247 Ala Ser Pro Asp Gln Glu Ile Ser Phe Ser Tyr Tyr Leu Ile Gly Lys
248             485             490             495
250 gga agt ttg gtg atg gag ggg cag aaa cac ctg aac tct aag aag aaa      1536
251 Gly Ser Leu Val Met Glu Gly Gln Lys His Leu Asn Ser Lys Lys Lys
252         500             505             510
254 gga ctg aaa gcc tcc ttc tct ctc tca ctg acc ttc act tcg aga ctg      1584
255 Gly Leu Lys Ala Ser Phe Ser Leu Ser Leu Thr Phe Thr Ser Arg Leu
256         515             520             525
258 gcc cct gat cct tcc ctg gtg atc tat gcc att ttt ccc agt gga ggt      1632
259 Ala Pro Asp Pro Ser Leu Val Ile Tyr Ala Ile Phe Pro Ser Gly Gly
260         530             535             540
262 gtt gta gct gac aaa att cag ttc tca gtc ggg atg tgc ttt gac aat      1680
263 Val Val Ala Asp Lys Ile Gln Phe Ser Val Gly Met Cys Phe Asp Asn
264 545             550             555             560
266 cag gtt tcc ctt ggc ttc tcc ccc tcc cag cag ctt cca gga gca gaa      1728
267 Gln Val Ser Leu Gly Phe Ser Pro Ser Gln Gln Leu Pro Gly Ala Glu
268             565             570             575
270 gtg gag ctg cag ctg cag gca gct ccc gga tcc ctg tgt gcg ctc cgg      1776
271 Val Glu Leu Gln Leu Gln Ala Ala Pro Gly Ser Leu Cys Ala Leu Arg
272         580             585             590
274 gcg gtg gat gag agt gtc tta ctg ctt agg cca gac aga gag ctg agc      1824
275 Ala Val Asp Glu Ser Val Leu Leu Leu Arg Pro Asp Arg Glu Leu Ser
276         595             600             605
278 aac cgc tct gtc tat ggg atg ttt cca ttc tgg tat ggt cac tac ccc      1872
279 Asn Arg Ser Val Tyr Gly Met Phe Pro Phe Trp Tyr Gly His Tyr Pro
280     610             615             620
282 tat caa gtg gct gag tat gat cag tgt cca gtg tct ggc cca tgg gac      1920
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283 Tyr Gln Val Ala Glu Tyr Asp Gln Cys Pro Val Ser Gly Pro Trp Asp
284 625                 630             635             640
286 ttt cct cag ccc ctc att gac cca atg ccc caa ggg cat tcg agc cag       1968
287 Phe Pro Gln Pro Leu Ile Asp Pro Met Pro Gln Gly His Ser Ser Gln
288                 645             650             655
290 cgt tcc att atc tgg agg ccc tcg ttc tct gaa ggc acg gac ctt ttc       2016
291 Arg Ser Ile Ile Trp Arg Pro Ser Phe Ser Glu Gly Thr Asp Leu Phe
292                 660             665             670
294 agc ttt ttc cgg gac gtg ggc ctg aaa ata ctg tcc aat gcc aaa atc       2064
295 Ser Phe Phe Arg Asp Val Gly Leu Lys Ile Leu Ser Asn Ala Lys Ile
296                 675             680             685
298 aag aag cca gta gat tgc agt cac aga tct cca gaa tac agc act gct       2112
299 Lys Lys Pro Val Asp Cys Ser His Arg Ser Pro Glu Tyr Ser Thr Ala
300                 690             695             700
302 atg ggt ggc ggt ggt cat cca gag gct ttt gag tca tca act cct tta       2160
303 Met Gly Gly Gly Gly His Pro Glu Ala Phe Glu Ser Ser Thr Pro Leu
304 705                 710             715             720
306 cat caa gca gag gat tct cag gtc cgc cag tac ttc cca gag acc tgg       2208
307 His Gln Ala Glu Asp Ser Gln Val Arg Gln Tyr Phe Pro Glu Thr Trp
308                 725             730             735
310 ctc tgg gat ctg ttt cct att ggt aac tcg ggg aag gag gcg gtc cac       2256
311 Leu Trp Asp Leu Phe Pro Ile Gly Asn Ser Gly Lys Glu Ala Val His
312                 740             745             750
314 gtc aca gtt cct gac gcc atc acc gag tgg aag gcg atg agt ttc tgc       2304
315 Val Thr Val Pro Asp Ala Ile Thr Glu Trp Lys Ala Met Ser Phe Cys
316                 755             760             765
318 act tcc cag tca aga ggc ttc ggg ctt tca ccc act gtt gga cta act       2352
319 Thr Ser Gln Ser Arg Gly Phe Gly Leu Ser Pro Thr Val Gly Leu Thr
320                 770             775             780
322 gct ttc aag ccg ttc ttt gtt gac ctg act ctc cct tac tca gta gtc       2400
323 Ala Phe Lys Pro Phe Phe Val Asp Leu Thr Leu Pro Tyr Ser Val Val
324 785                 790             795             800
326 cgt ggg gaa tcc ttt cgt ctt act gcc acc atc ttc aat tac cta aag       2448
327 Arg Gly Glu Ser Phe Arg Leu Thr Ala Thr Ile Phe Asn Tyr Leu Lys
328                 805             810             815
330 gat tgc atc agg gtt cag act gac ctg gct aaa tcg cat gag tac cag       2496
331 Asp Cys Ile Arg Val Gln Thr Asp Leu Ala Lys Ser His Glu Tyr Gln
332                 820             825             830
334 cta gaa tca tgg gca gat tct cag acc tcc agt tgt ctc tgt gct gat       2544
335 Leu Glu Ser Trp Ala Asp Ser Gln Thr Ser Ser Cys Leu Cys Ala Asp
336                 835             840             845
338 gac gca aaa acc cac cac tgg aac atc aca gct gtc aaa ttg ggt cac       2592
339 Asp Ala Lys Thr His His Trp Asn Ile Thr Ala Val Lys Leu Gly His
340     850                 855             860
342 att aac ttt act att agt aca aag att ctg gac agc aat gaa cca tgt       2640
343 Ile Asn Phe Thr Ile Ser Thr Lys Ile Leu Asp Ser Asn Glu Pro Cys
344 865                 870             875             880
346 ggg ggc cag aag ggg ttt gtt ccc caa aag ggc cga agt gac acg ctc       2688
347 Gly Gly Gln Lys Gly Phe Val Pro Gln Lys Gly Arg Ser Asp Thr Leu
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FYI:

Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY   DATE: 01/25/2001
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L:20 M:270 C: Current Application Number differs, Replaced Current Application Number
L:2277 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:26